SEQUENCE LISTING

<110> BARTOSCH et al.

<120> Infectious pestivirus pseudo-particles containing functional Erns, E1
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<130> P08199US00/BAS

<140> US 10/791.283
<141> 2004-03-03

<150> EP 03290506.9
<151> 2003-03-03

<160> 26

<170> PatentIn version 3.2

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Lys Glu Glu Gly Ala Thr Lys Lys Lys Thr Gln Lys Pro Asp Arg Leu
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gaa agg ggg aaa atg aaa ata gtg ccc aaa gaa tct gaa aaa gac agc      994
Glu Arg Gly Lys Met Lys Ile Val Pro Lys Glu Ser Glu Lys Asp Ser
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aaa act aaa cct ccg gat gct aca ata gtg gtg gaa gga gtc aaa tac     1042
Lys Thr Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly Val Lys Tyr
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Gln Val Arg Lys Lys Gly Lys Thr Lys Ser Lys Asn Thr Gln Asp Gly
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ttg tac cat aac aaa aac aaa cct cag gaa tca cgc aag aaa ctg gaa     1138
Leu Tyr His Asn Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu
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aaa gca ttg ttg gcg tgg gca ata ata gct ata gtt ttg ttt caa gtt     1186
Lys Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val
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Thr Met Gly Glu Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr
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gaa ggg ata caa cgg gca atg ttc caa agg ggt gtg aat aga agt tta     1282
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His Gly Ile Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu
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gcc acc gat ata gaa cta aaa aca att cat ggt atg atg gat gca agt        1378
Ala Thr Asp Ile Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser
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gag aag acc aac tac acg tgt tgc aga ctt caa cgc cat gag tgg aac        1426
Glu Lys Thr Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn
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Lys His Gly Trp Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val
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Met Asn Arg Thr Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu
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Cys Ala Val Thr Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val
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aca caa gct aga gat agc ccc aca ccc tta aca ggt tgc aag aaa gga        1618
Thr Gln Ala Arg Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly
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Lys Asn Phe Ser Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe
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gaa ata gct gca agt gat gta tta ttc aaa gaa cat gaa cgc att agt        1714
Glu Ile Ala Ala Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser
260             265             270             275

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Met Phe Gln Asp Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser
            280             285             290

tta gaa ggt gcc aga caa gga acc gct aaa ctg aca acc tgg tta ggc        1810
Leu Glu Gly Ala Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly
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aag cag ctc ggg ata cta gga aaa aag ttg gaa aac aag agt aag acg        1858
Lys Gln Leu Gly Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr
            310             315             320

tgg ttt gga gca tac gct gct tcc cct tac tgt gat gtc gat cgc aaa        1906
Trp Phe Gly Ala Tyr Ala Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys
            325             330             335

att ggc tac ata tgg tat aca aaa aat tgc acc cct gcc tgc tta ccc        1954
Ile Gly Tyr Ile Trp Tyr Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro
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Lys Asn Thr Lys Ile Val Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu
            360                 365                 370

gac ggc aag ata tta cat gag atg ggg ggt cac ttg tcg gag gta cta        2050
Asp Gly Lys Ile Leu His Glu Met Gly Gly His Leu Ser Glu Val Leu
            375                 380                 385

cta ctt tct tta gtg gtg ctg tcc gac ttc gca ccg gaa aca gct agt        2098
Leu Leu Ser Leu Val Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser
            390                 395                 400

gta atg tac cta atc cta cat ttt tcc atc cca caa agt cac gtt gat        2146
Val Met Tyr Leu Ile Leu His Phe Ser Ile Pro Gln Ser His Val Asp
        405                 410                 415

gta atg gat tgt gat aag acc cag ttg aac ctc aca gtg gag ctg aca        2194
Val Met Asp Cys Asp Lys Thr Gln Leu Asn Leu Thr Val Glu Leu Thr
420                 425                 430                 435

aca gct gaa gta ata cca ggg tcg gtc tgg aat cta ggc aaa tat gta        2242
Thr Ala Glu Val Ile Pro Gly Ser Val Trp Asn Leu Gly Lys Tyr Val
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Cys Ile Arg Pro Asn Trp Trp Pro Tyr Glu Thr Thr Val Val Leu Ala
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ttt gaa gag gtg agc cag gtg gtg aag tta gtg ttg agg gca ctc aga        2338
Phe Glu Glu Val Ser Gln Val Val Lys Leu Val Leu Arg Ala Leu Arg
            470                 475                 480

gat tta aca cgc att tgg aac gct gca aca act act gct ttt tta gta        2386
Asp Leu Thr Arg Ile Trp Asn Ala Ala Thr Thr Thr Ala Phe Leu Val
        485                 490                 495

tgc ctt gtt aag ata gtc agg ggc cag atg gta cag ggc att ctg tgg        2434
Cys Leu Val Lys Ile Val Arg Gly Gln Met Val Gln Gly Ile Leu Trp
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cta cta ttg ata aca ggg gta caa ggg cac ttg gat tgc aaa cct gaa        2482
Leu Leu Leu Ile Thr Gly Val Gln Gly His Leu Asp Cys Lys Pro Glu
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Phe Ser Tyr Ala Ile Ala Lys Asp Glu Arg Ile Gly Gln Leu Gly Ala
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gaa ggc ctt acc acc act tgg aag gaa tac tca cct gga atg aag ctg        2578
Glu Gly Leu Thr Thr Thr Trp Lys Glu Tyr Ser Pro Gly Met Lys Leu
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gaa gac aca atg gtc att gct tgg tgc gaa gat ggg aag tta atg tac        2626
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aga gcc ttg ccg acc agt gtg gta ttc aaa aaa ctc ttt gat ggg cga    2722
Arg Ala Leu Pro Thr Ser Val Val Phe Lys Lys Leu Phe Asp Gly Arg
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aag caa gag gat gta gtc gaa atg aac gac aac ttt gaa ttt gga ctc    2770
Lys Gln Glu Asp Val Val Glu Met Asn Asp Asn Phe Glu Phe Gly Leu
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ctg ctg aac gga ccg gcc ttc cag atg gta tgc ccc ata gga tgg aca    2866
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Val Val Arg Thr Tyr Arg Arg Ser Lys Pro Phe Pro His Arg Gln Gly
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Cys Ile Thr Gln Lys Asn Leu Gly Glu Asp Leu His Asn Cys Ile Leu
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Gly Gly Asn Trp Thr Cys Val Pro Gly Asp Gln Leu Leu Tyr Lys Gly
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Gly Ser Ile Glu Ser Cys Lys Trp Cys Gly Tyr Gln Phe Lys Glu Ser
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gag gga cta cca cac tac ccc att ggc aag tgt aaa ttg gag aac gag    3154
Glu Gly Leu Pro His Tyr Pro Ile Gly Lys Cys Lys Leu Glu Asn Glu
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act ggt tac agg cta gta gac agt acc tct tgc aat aga gaa ggt gtg    3202
Thr Gly Tyr Arg Leu Val Asp Ser Thr Ser Cys Asn Arg Glu Gly Val
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Ala Ile Val Pro Gln Gly Thr Leu Lys Cys Lys Ile Gly Lys Thr Thr
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Val Gln Val Ile Ala Met Asp Thr Lys Leu Gly Pro Met Pro Cys Arg
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Pro Tyr Glu Ile Ile Ser Ser Glu Gly Pro Val Glu Lys Thr Ala Cys
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gac agc tac ttt cag caa tac atg cta aaa gga gag tat caa tac tgg        3442
Asp Ser Tyr Phe Gln Gln Tyr Met Leu Lys Gly Glu Tyr Gln Tyr Trp
                840                 845                 850

ttt gac ctg gag gtg act gac cat cac cgg gat tac ttc gct gag tcc        3490
Phe Asp Leu Glu Val Thr Asp His His Arg Asp Tyr Phe Ala Glu Ser
            855                 860                 865

ata tta gtg gtg gta gta gcc ctc ttg ggt ggc aga tat gta ctt tgg       3538
Ile Leu Val Val Val Val Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp
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Leu Leu Val Thr Tyr Met Val Leu Ser Glu Gln Lys Ala Leu Gly Ile
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cag tat gga tca ggg gaa gtg gtg atg atg ggc aac ttg cta acc cat       3634
Gln Tyr Gly Ser Gly Glu Val Val Met Met Gly Asn Leu Leu Thr His
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Arg Glu Glu Ser Val Lys Lys Trp Val Leu Leu Leu Tyr His Ile Leu
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aggtagagca ctactacaaa ggggtcacag caaaaattga ctacagtaaa ggaaaaatgc     9113

tcttggccac tgacaagtgg gaggtggaac atggtgtcat aaccaggtta gctaagagat     9173

atactggggt cgggttcaat ggtgcatact taggtgacga gcccaatcac cgtgctctag     9233

tggagaggga ctgtgcaact ataaccaaaa acacagtaca gtttctaaaa atgaagaagg     9293

ggtgtgcgtt cacctatgac ctgaccatct ccaatctgac caggctcatc gaactagtac     9353

acaggaacaa tcttgaagag aaggaaatac ccaccgctac ggtcaccaca tggctagctt     9413
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acaccttcgt gaatgaagac gtagggacta taaaaccagt actaggagag agagtaatcc   9473

ccgaccctgt agttgatatc aatttacaac cagaggtgca agtggacacg tcagaggttg   9533

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aagtagagcc tgacgccagc gacaaccaaa actcggtgaa gatcgggttg gatgagggta   9653

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cgaggccctt catcatgatc ctgggctcaa ggaattccat atcaaatagg gcaaagactg   9773

ctagaaatat aaatctgtac acaggaaatg accccaggga aatacgagac ttgatggctg   9833

cagggcgcat gttagtagta gcactgaggg atgtcgaccc tgagctgtct gaaatggtcg   9893

atttcaaggg gactttttta gatagggagg ccctggaggc tctaagtctc gggcaaccta   9953

aaccgaagca ggttaccaag gaagctgtta ggaatttgat agaacagaaa aaagatgtgg   10013

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ataagtacta cttagtagga gatgttggag agctaaaaga tcaagctaaa gcacttgggg   10133

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taccaaaaaa tgagaagaga gatgtcagtg atgactggca ggcaggggac ctggtggttg   11033

agaagaggcc aagagttatc caataccctg aagccaagac aaggctagcc atcactaagg   11093

tcatgtataa ctgggtgaaa cagcagcccg ttgtgattcc aggatatgaa ggaaagaccc   11153
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ccttgttcaa catctttgat aaagtgagaa aggaatggga ctcgttcaat gagccagtgg   11213

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ccgaccacat gacagaagta ccagttataa cagcagatgg tgaagtatat ataagaaatg   11393

ggcagagagg gagcggccag ccagacacaa gtgctggcaa cagcatgtta aatgtcctga   11453

caatgatgta cggcttctgc gaaagcacag gggtaccgta caagagtttc aacagggtgg   11513

caaggatcca cgtctgtggg gatgatggct tcttaataac tgaaaaaggg ttagggctga   11573

aatttgctaa caaagggatg cagattcttc atgaagcagg caaacctcag aagataacgg   11633

aaggggaaaa gatgaaagtt gcctatagat ttgaggatat agagttctgt tctcataccc   11693

cagtccctgt taggtggtcc gacaacacca gtagtcacat ggccgggaga gacaccgctg   11753

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ggaccgtcca cctcaagaag acgacacgcc caacacgcac agctaaacag tagtcaagat   12473

tatctacctc aagataacac tacatttaat gcacacagca ctttagctgt atgaggatac   12533

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<210> 2
<211> 102
<212> PRT
<213> Bovine viral diarrhea virus

<400> 2

Ser Asp Thr Lys Glu Glu Gly Ala Thr Lys Lys Lys Thr Gln Lys Pro
1   5   10   15

Asp Arg Leu Glu Arg Gly Lys Met Lys Ile Val Pro Lys Glu Ser Glu
                20   25   30

Lys Asp Ser Lys Thr Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly
            35   40   45

Val Lys Tyr Gln Val Arg Lys Lys Gly Lys Thr Lys Ser Lys Asn Thr
    50   55   60

Gln Asp Gly Leu Tyr His Asn Lys Asn Lys Pro Gln Glu Ser Arg Lys
65   70   75   80

Lys Leu Glu Lys Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Val Leu
                85   90   95

Phe Gln Val Thr Met Gly
            100

<210>   3
<211>   227
<212>   PRT
<213>   Bovine viral diarrhea virus

<400>   3

Glu Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu Gly Ile
1   5   10   15

Gln Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile
                20   25   30

Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala Thr Asp
            35   40   45

Ile Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu Lys Thr
    50   55   60

Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys His Gly
65   70   75   80

Trp Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met Asn Arg
                85   90   95

Thr Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys Ala Val
            100   105   110

Thr Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val Thr Gln Ala
            115   120   125

Arg Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe
            130   135   140

Ser Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe Glu Ile Ala
145   150   155   160

Ala Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser Met Phe Gln
                165   170   175

Asp Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser Leu Glu Gly
            180   185   190

Ala Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly Lys Gln Leu
            195   200   205

Gly Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr Trp Phe Gly
            210   215   220

Ala Tyr Ala
225

<210>   4
<211>   195
<212>   PRT
<213>   Bovine viral diarrhea virus

<400>   4

Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr
1   5   10   15

Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val
            20   25   30

Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His
            35   40   45

Glu Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val
    50   55   60

Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu
65   70   75   80

His Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys
            85   90   95

Thr Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro
        100   105   110

Gly Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp
        115   120   125

Trp Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln
    130   135   140

Val Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp
145   150   155   160

Asn Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val
            165   170   175

Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly
            180   185   190

Val Gln Gly
        195

<210> 5
<211> 374
<212> PRT
<213> Bovine viral diarrhea virus

<400> 5

His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys Asp Glu
1   5   10   15

Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp Lys Glu
            20   25   30

Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala Trp Cys
        35   40   45

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Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu Thr Arg
    50              55              60

Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val Val Phe
65              70              75              80

Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu Met Asn
            85              90              95

Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro Ile Val
            100             105             110

Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe Gln Met
        115             120             125

Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser Phe Asn
    130             135             140

Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg Ser Lys
145             150             155             160

Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu Gly Glu
            165             170             175

Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val Pro Gly
            180             185             190

Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys Trp Cys
        195             200             205

Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro Ile Gly
    210             215             220

Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp Ser Thr
225             230             235             240

Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr Leu Lys
            245             250             255

Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp Thr Lys
            260             265             270
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Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser Glu Gly
        275   280   285

Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr Leu Lys
        290   295   300

Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu
305   310   315   320

Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp His His
                325   330   335

Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala Leu Leu
            340   345   350

Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val Leu Ser
            355   360   365

Glu Gln Lys Ala Leu Gly
        370

<210>   6
<211>   70
<212>   PRT
<213>   Bovine viral diarrhea virus

<400>   6

Ile Gln Tyr Gly Ser Gly Glu Val Val Met Met Gly Asn Leu Leu Thr
1   5   10   15

His Asn Asn Ile Glu Val Val Thr Tyr Phe Leu Leu Leu Tyr Leu Leu
            20   25   30

Leu Arg Glu Glu Ser Val Lys Lys Trp Val Leu Leu Leu Tyr His Ile
        35   40   45

Leu Val Val His Pro Ile Lys Ser Val Ile Val Ile Leu Leu Met Ile
        50   55   60

Gly Asp Val Val Lys Ala
65   70

<210>   7

<211> 12301
<212> DNA
<213> Swine fever virus

<220>
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<222> (878)..(1174)
<223> core protein

<220>
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<222> (1175)..(1855)
<223> E-rns protein

<220>
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<222> (1856)..(2440)
<223> E1 protein

<220>
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<222> (2441)..(3559)
<223> E2 protein

<220>
<221> CDS
<222> (3560)..(3769)
<223> p7 protein

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gtatacgagg ttagttcatt ctcgtatgca tgattggaca aatcaaaatt tcaatttggt   60

tcagggcctc cctccagcga cggccgaact gggctagcca tgcccacagt aggactagca   120

aacggaggga ctagccgtag tggcgagctc cctgggtggt ctaagtcctg agtacaggac   180

agtcgtcagt agttcgacgt gagcagaagc ccacctcgag atgctatgtg gacgagggca   240

tgcccaagac acaccttaac cctagcgggg gtcgctaggg tgaaatcaca ccacgtgatg   300

ggagtacgac ctgatagggc gctgcagagg cccactatta ggctagtata aaaatctctg   360

ctgtacatgg cacatggagt tgaatcattt tgaacttttta tacaaaacaa acaaacaaaa   420

accaatggga gtggaggaac cggtatacga tgccacgggg aggccattgt ttggagaccc   480

gagtgaggta cacccacaat caacactgaa gctaccacat gatagggggga gaggtaacat   540

caaaacaaca ctgaagaacc tacctaggaa aggcgactgc aggagtggca accatctagg   600

cccggttagt gggatatatg taaagcccgg ccctgtcttt tatcaggact acatgggccc   660

ggtctaccat agagcccctc tagagttttt taacgaagcg cagttttgcg aggtgaccaa   720

aaggataggt agggtgacag gtagtgacgg aaagctttac catatatatg tgtgcatcga   780

tggttgcata ctgctgaagc tagccaagag ggacgagcca agaaccctga agtggattag   840

aaatttcacc gactgtccat tgtgggttac cagttgc tct gat gat ggc gca agt   895
                                         Ser Asp Asp Gly Ala Ser
                                         1   5

gga agt aaa gag aag aag cca gat agg atc aac aaa ggc aaa tta aaa   943
Gly Ser Lys Glu Lys Lys Pro Asp Arg Ile Asn Lys Gly Lys Leu Lys
            10   15   20

ata gcc cca aaa gag cat gag aag gac agc aga act aag cca cct gac   991
Ile Ala Pro Lys Glu His Glu Lys Asp Ser Arg Thr Lys Pro Pro Asp
        25   30   35

gct acg att gta gtg gaa gga gta aaa tac cag gtt aaa aag aag ggt   1039
Ala Thr Ile Val Val Glu Gly Val Lys Tyr Gln Val Lys Lys Lys Gly
    40   45   50

aaa gtt aaa gga aag agt acc caa gac ggc ctg tac cac aac aag aat   1087
Lys Val Lys Gly Lys Ser Thr Gln Asp Gly Leu Tyr His Asn Lys Asn
55   60   65   70

aaa cca cca gaa tct agg aag aaa tta gaa aaa gcc cta ttg gca tgg   1135
Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu Ala Trp
                75   80   85

gcg gta ata gca att atg ttg tac caa cca gtt gaa gcc gaa aat ata   1183
Ala Val Ile Ala Ile Met Leu Tyr Gln Pro Val Glu Ala Glu Asn Ile
            90   95   100

act caa tgg aac ctg agt gac aac ggc act aat ggt atc cag cat gct   1231
Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Asn Gly Ile Gln His Ala
            105   110   115

atg tac ctt aga ggg gtt agc agg agc ttg cat ggg atc tgg ccg gaa   1279
Met Tyr Leu Arg Gly Val Ser Arg Ser Leu His Gly Ile Trp Pro Glu
    120   125   130

aaa ata tgc aaa gga gtc ccc acc tac ctg gcc aca gac acg gaa ctg   1327
Lys Ile Cys Lys Gly Val Pro Thr Tyr Leu Ala Thr Asp Thr Glu Leu
135   140   145   150

aaa gaa ata cag gga atg atg gat gcc agc gag ggg aca aac tat acg   1375
Lys Glu Ile Gln Gly Met Met Asp Ala Ser Glu Gly Thr Asn Tyr Thr
                155   160   165

tgc tgt aag tta cag aga cat gaa tgg aac aaa cat gga tgg tgt aac   1423
Cys Cys Lys Leu Gln Arg His Glu Trp Asn Lys His Gly Trp Cys Asn
            170   175   180

tgg tac aat ata gac ccc tgg ata cag ttg atg aat aga acc caa gca   1471
Trp Tyr Asn Ile Asp Pro Trp Ile Gln Leu Met Asn Arg Thr Gln Ala
            185   190   195

aac ttg gca gaa ggc cct ccg gcc aag gag tgc gct gtg act tgc agg   1519
Asn Leu Ala Glu Gly Pro Pro Ala Lys Glu Cys Ala Val Thr Cys Arg
    200   205   210

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tac gat aaa gat gct gac atc aac gtg gtc acc cag gcc aga aac agg          1567
Tyr Asp Lys Asp Ala Asp Ile Asn Val Val Thr Gln Ala Arg Asn Arg
215             220             225             230

cca aca acc ctg acc ggt tgc aag aaa gga aaa aat ttt tct ttt gcg          1615
Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe Ser Phe Ala
                235             240             245

ggt aca gtt ata gag ggc cca tgt aat ttc aat gtt tcc gtg gag gat          1663
Gly Thr Val Ile Glu Gly Pro Cys Asn Phe Asn Val Ser Val Glu Asp
                250             255             260

atc ttg tat ggg gat cat gag tgc ggc agt ttg ctt cag gac acg gct          1711
Ile Leu Tyr Gly Asp His Glu Cys Gly Ser Leu Leu Gln Asp Thr Ala
                265             270             275

ctg tac cta gtg gat gga atg acc aac act ata gag aat gcc aga cag          1759
Leu Tyr Leu Val Asp Gly Met Thr Asn Thr Ile Glu Asn Ala Arg Gln
                280             285             290

gga gca gcg agg gta aca tct tgg ctc ggg agg caa ctc agc act gcc          1807
Gly Ala Ala Arg Val Thr Ser Trp Leu Gly Arg Gln Leu Ser Thr Ala
295             300             305             310

ggg aag agg ttg gag ggt aga agc aaa acc tgg ttt ggt gcc tat gcc          1855
Gly Lys Arg Leu Glu Gly Arg Ser Lys Thr Trp Phe Gly Ala Tyr Ala
                315             320             325

cta tcg cct tac tgt aat gta aca agc aaa ata ggg tac ata tgg tac          1903
Leu Ser Pro Tyr Cys Asn Val Thr Ser Lys Ile Gly Tyr Ile Trp Tyr
                330             335             340

act aac aac tgc acc ccg gct tgc ctc ccc aaa aat aca aag ata ata          1951
Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile
                345             350             355

ggc ccc gga aaa ttt gac act aac gcg gaa gac gga aag att ctc cat          1999
Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His
    360             365             370

gag atg ggg ggt cac cta tca gaa ttt ctg ctg ctc tct ctg gtt gtt          2047
Glu Met Gly Gly His Leu Ser Glu Phe Leu Leu Leu Ser Leu Val Val
375             380             385             390

ctg tct gac ttc gcc cct gaa aca gcc agc gcg tta tac ctc att ttg          2095
Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Ala Leu Tyr Leu Ile Leu
                395             400             405

cac tac atg att cct caa tcc cat gaa gaa cct gaa ggc tgc gac aca          2143
His Tyr Met Ile Pro Gln Ser His Glu Glu Pro Glu Gly Cys Asp Thr
                410             415             420

aac cag ctg aat cta aca gtg gaa ctc agg act gaa gac gta ata ccg          2191
Asn Gln Leu Asn Leu Thr Val Glu Leu Arg Thr Glu Asp Val Ile Pro
    425             430             435
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tca tca gtc tgg aat gtt ggc aaa tat gtg tgt gtt aga cca gac tgg      2239
Ser Ser Val Trp Asn Val Gly Lys Tyr Val Cys Val Arg Pro Asp Trp
    440                 445                 450

tgg cca tat gaa acc aag gtg gct ttg tta ttt gaa gag gca gga cag      2287
Trp Pro Tyr Glu Thr Lys Val Ala Leu Leu Phe Glu Glu Ala Gly Gln
455                 460                 465                 470

gtc gta aaa tta gcc tta cga gcg ctg agg gat tta acc agg gtc tgg      2335
Val Val Lys Leu Ala Leu Arg Ala Leu Arg Asp Leu Thr Arg Val Trp
                475                 480                 485

aat agc gca tca acc acg gca ttc ctc atc tgc ttg ata aaa gta tta      2383
Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Ile Lys Val Leu
                490                 495                 500

aga gga cag atc gtg caa ggt gtg ata tgg ctg cta cta gta act ggg      2431
Arg Gly Gln Ile Val Gln Gly Val Ile Trp Leu Leu Leu Val Thr Gly
        505                 510                 515

gca caa ggc cgg cta gcc tgc aag gaa gat tac agg tac gca ata tca      2479
Ala Gln Gly Arg Leu Ala Cys Lys Glu Asp Tyr Arg Tyr Ala Ile Ser
    520                 525                 530

tcg acc aat gag ata ggg cta ctc ggg gcc gaa ggt ctc acc acc acc      2527
Ser Thr Asn Glu Ile Gly Leu Leu Gly Ala Glu Gly Leu Thr Thr Thr
535                 540                 545                 550

tgg aaa gaa tac aac cac gat ttg caa ctg aat gac ggg acc gtt aag      2575
Trp Lys Glu Tyr Asn His Asp Leu Gln Leu Asn Asp Gly Thr Val Lys
                555                 560                 565

gcc att tgc gtg gca ggt tcc ttt aaa gtc ata gca ctt aat gtg gtc      2623
Ala Ile Cys Val Ala Gly Ser Phe Lys Val Ile Ala Leu Asn Val Val
                570                 575                 580

agt agg agg tat ttg gca tca ttg cat aag gag gct tca ctc act tcc      2671
Ser Arg Arg Tyr Leu Ala Ser Leu His Lys Glu Ala Ser Leu Thr Ser
        585                 590                 595

gtg aca ttt gag ctc ctg ttc gac ggg acc aac cca tca act gag gaa      2719
Val Thr Phe Glu Leu Leu Phe Asp Gly Thr Asn Pro Ser Thr Glu Glu
    600                 605                 610

atg gga gat gac ttc ggg ttc ggg ctg tgc ccg ttc gat acg agt cct      2767
Met Gly Asp Asp Phe Gly Phe Gly Leu Cys Pro Phe Asp Thr Ser Pro
615                 620                 625                 630

gtt gtc aag gga aag tac aat aca acc ttg ttg aac ggt agt gct ttc      2815
Val Val Lys Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe
                635                 640                 645

tat ctt gtc tgc cca ata ggg tgg acg ggt gtc ata gag tgc aca gca      2863
Tyr Leu Val Cys Pro Ile Gly Trp Thr Gly Val Ile Glu Cys Thr Ala
                650                 655                 660

gtg agc cca aca act ctg aga aca gaa gtg gta aag acc ttc agg aga      2911
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Val Ser Pro Thr Thr Leu Arg Thr Glu Val Val Lys Thr Phe Arg Arg
        665             670             675

gac aag ccc ttt ccg cac aga atg gat tgt gcg acc acc aca gtg gaa   2959
Asp Lys Pro Phe Pro His Arg Met Asp Cys Ala Thr Thr Thr Val Glu
        680             685             690

aat gga gat tta ttc tac tgt aag ttg ggg ggc aac tgg aca tgt gtg   3007
Asn Gly Asp Leu Phe Tyr Cys Lys Leu Gly Gly Asn Trp Thr Cys Val
695             700             705             710

aaa ggt gaa cca gtg gtc tac acg ggg ggg cta gta aaa caa tgc aga   3055
Lys Gly Glu Pro Val Val Tyr Thr Gly Gly Leu Val Lys Gln Cys Arg
                715             720             725

tgg tgt ggc ttc gac ttc aat gag ccc gac gga ctc ccg cac tac ccc   3103
Trp Cys Gly Phe Asp Phe Asn Glu Pro Asp Gly Leu Pro His Tyr Pro
            730             735             740

ata ggt aag tgc atc ttg gta aat gag aca ggt tac aga ata gta gat   3151
Ile Gly Lys Cys Ile Leu Val Asn Glu Thr Gly Tyr Arg Ile Val Asp
            745             750             755

tca acg gac tgt aac aga gat ggc gtt gta atc agc aca gat ggg agt   3199
Ser Thr Asp Cys Asn Arg Asp Gly Val Val Ile Ser Thr Asp Gly Ser
        760             765             770

cat gag tgc ttg atc ggt aac aca act gtc aag gtg cat gca tca gat   3247
His Glu Cys Leu Ile Gly Asn Thr Thr Val Lys Val His Ala Ser Asp
775             780             785             790

gaa aga ctg ggc cct atg cca tgc aga ccc aaa gag att gtc tct agt   3295
Glu Arg Leu Gly Pro Met Pro Cys Arg Pro Lys Glu Ile Val Ser Ser
                795             800             805

gca gga cct gta agg aaa act tcc tgt aca ttc aac tac gca aaa act   3343
Ala Gly Pro Val Arg Lys Thr Ser Cys Thr Phe Asn Tyr Ala Lys Thr
                810             815             820

ttg aag aac aag tac tat gag ccc agg gac agc tac ttc cag caa tat   3391
Leu Lys Asn Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr
        825             830             835

atg ctt aag ggc gag tat cag tac tgg ttt gac ctg gac gtg act gac   3439
Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Asp Val Thr Asp
        840             845             850

cgc cac tca gat tac ttc gca gaa ttt gtc gtc ttg gta gtg gta gca   3487
Arg His Ser Asp Tyr Phe Ala Glu Phe Val Val Leu Val Val Val Ala
855             860             865             870

ctg tta gga gga aga tat gtc ctg tgg cta ata gtg acc tac ata gtt   3535
Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Ile Val Thr Tyr Ile Val
                875             880             885

cta aca gaa caa ctc gcc gct ggt tta cca ttg ggc cag ggt gag gta   3583
Leu Thr Glu Gln Leu Ala Ala Gly Leu Pro Leu Gly Gln Gly Glu Val
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gtg ttg ata ggg aac tta att acc cac aca gac att gag gtc gta gta    3631
Val Leu Ile Gly Asn Leu Ile Thr His Thr Asp Ile Glu Val Val Val
        905                 910                 915

tat ttc tta cta ctc tat ttg gtc atg agg gat gag cct ata aag aaa    3679
Tyr Phe Leu Leu Leu Tyr Leu Val Met Arg Asp Glu Pro Ile Lys Lys
    920                 925                 930

tgg ata ctg ctg ctg ttc cat gct atg act aac aat cca gtc aag acc    3727
Trp Ile Leu Leu Leu Phe His Ala Met Thr Asn Asn Pro Val Lys Thr
935             940                 945                 950

ata aca gtg gca ttg ctt atg gtt agt ggg gtt gcc aag ggt            3769
Ile Thr Val Ala Leu Leu Met Val Ser Gly Val Ala Lys Gly
            955                 960
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ggaaagatag acggcggttg gcagcggctg ccagagacca gctttgacat ccaactcgcg    3829

ctgacagtta tagtagtcgc tgtgatgtta ctggcaaaga gagatccaac tactgtcccc    3889

ttggttataa cagtggcaac cctgagaacg gctaagatga ctaatggact tagcacggat    3949

atagccatag ctacagtgtc aacagcgttg ctaacctgga cctacattag tgactattat    4009

agatacaaga cttggctaca gtaccttatt agcacagtga caggtatctt cttaataagg    4069

gtactgaagg gaataggtga gttggattta cacactccaa ccttgccatc ttacagaccc    4129

ctcttcttca ttctcgtgta cctcatttcc actgcagtgg taacaagatg gaatctggac    4189

atagccggat tgctgttgca gtgtgtccca acccttttga tggtttttac gatgtgggca    4249

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aacgacatat acgaagttga ccaatctggt gaaggggttt accttttccc gtcaaaacaa    4429

aagacaagtt caataacagg taccatgttg ccattgatca aagccatact catcagctgc    4489

atcagtaata agtggcagtt catatatcta ttgtacttga tatttgaagt gtcttactac    4549

ctccacaaga agatcataga tgaaatagca ggagggacca acttcatctc aagacttgta    4609

gccgctttga tcgaagccaa ttgggccttt gacaacgaag aagttagggg tttaaagaag    4669

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gtaatggtcc actggtttgg tgacgaagag gtttatggga tgccaaagtt ggttggctta    4789

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agagagtgga gaggagaaac ctgcccaaaa tgcgggcgtt ttgggccacc aatgacctgt    4909

ggtatgaccc tagccgactt tgaagaaaaa cattataaga ggatcttttt tagagaggat    4969
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caattattcc tgaggaatct cccggtgcta gcaacaaaag tcaagatgct cctggtcgga      5089

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atagggaggc ataagagagt cttggtcttg atccctctga gggcggcagc agagtcagta      5929

taccaatata tgagacaaaa acatccaagc atcgcattta acctgaggat aggggagatg      5989

aaggaagggg acatggccac agggataacc tatgcttcat acggttactt ctgtcagatg      6049

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gatgtggttg tcgatacagg gcttaagtgt gaaaagagaa tacggctgtc acctaagatg      6589

cccttcatag tgacgggcct gaagagaatg gctgtcacga ttggggaaca agcccagaga      6649
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caaaggacag ccggtaggaa ccttttcact ttgataatgt tcgaggctgt ggaactactg    8389
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gcaaaagtgt attctatgaa actgagtaat tgggtgatgc aagaagaaaa taaacagggc    9949

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tgggatcaat tccaaaatcc agtggcagtg agttttgaca ctaaggcgtg ggacacccag   10969

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<210> 8
<211> 99
<212> PRT
<213> Swine fever virus

<400> 8

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Ser Asp Asp Gly Ala Ser Gly Ser Lys Glu Lys Lys Pro Asp Arg Ile
1               5                   10                  15


Asn Lys Gly Lys Leu Lys Ile Ala Pro Lys Glu His Glu Lys Asp Ser
            20                  25                  30


Arg Thr Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly Val Lys Tyr
            35                  40                  45


Gln Val Lys Lys Lys Gly Lys Val Lys Gly Lys Ser Thr Gln Asp Gly
        50                  55                  60


Leu Tyr His Asn Lys Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu
65                  70                  75                  80


Lys Ala Leu Leu Ala Trp Ala Val Ile Ala Ile Met Leu Tyr Gln Pro
                85                  90                  95


Val Glu Ala
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<210> 9
<211> 227
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<212> PRT
<213> Swine fever virus

<400> 9

Glu Asn Ile Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Asn Gly Ile
1               5                   10                  15

Gln His Ala Met Tyr Leu Arg Gly Val Ser Arg Ser Leu His Gly Ile
            20                  25                  30

Trp Pro Glu Lys Ile Cys Lys Gly Val Pro Thr Tyr Leu Ala Thr Asp
        35                  40                  45

Thr Glu Leu Lys Glu Ile Gln Gly Met Met Asp Ala Ser Glu Gly Thr
    50                  55                  60

Asn Tyr Thr Cys Cys Lys Leu Gln Arg His Glu Trp Asn Lys His Gly
65                  70                  75                  80

Trp Cys Asn Trp Tyr Asn Ile Asp Pro Trp Ile Gln Leu Met Asn Arg
            85                  90                  95

Thr Gln Ala Asn Leu Ala Glu Gly Pro Pro Ala Lys Glu Cys Ala Val
            100                 105                 110

Thr Cys Arg Tyr Asp Lys Asp Ala Asp Ile Asn Val Val Thr Gln Ala
        115                 120                 125

Arg Asn Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe
    130                 135                 140

Ser Phe Ala Gly Thr Val Ile Glu Gly Pro Cys Asn Phe Asn Val Ser
145                 150                 155                 160

Val Glu Asp Ile Leu Tyr Gly Asp His Glu Cys Gly Ser Leu Leu Gln
                165                 170                 175

Asp Thr Ala Leu Tyr Leu Val Asp Gly Met Thr Asn Thr Ile Glu Asn
            180                 185                 190

Ala Arg Gln Gly Ala Ala Arg Val Thr Ser Trp Leu Gly Arg Gln Leu
            195                 200                 205

Ser Thr Ala Gly Lys Arg Leu Glu Gly Arg Ser Lys Thr Trp Phe Gly
    210                 215             220

Ala Tyr Ala
225


<210>   10
<211>   195
<212>   PRT
<213>   Swine fever virus

<400>   10

Leu Ser Pro Tyr Cys Asn Val Thr Ser Lys Ile Gly Tyr Ile Trp Tyr
1               5               10              15

Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile
            20              25              30

Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His
        35              40              45

Glu Met Gly Gly His Leu Ser Glu Phe Leu Leu Leu Ser Leu Val Val
    50              55              60

Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Ala Leu Tyr Leu Ile Leu
65              70              75                      80

His Tyr Met Ile Pro Gln Ser His Glu Glu Pro Glu Gly Cys Asp Thr
                85              90              95

Asn Gln Leu Asn Leu Thr Val Glu Leu Arg Thr Glu Asp Val Ile Pro
            100             105             110

Ser Ser Val Trp Asn Val Gly Lys Tyr Val Cys Val Arg Pro Asp Trp
        115             120             125

Trp Pro Tyr Glu Thr Lys Val Ala Leu Leu Phe Glu Glu Ala Gly Gln
    130             135             140

Val Val Lys Leu Ala Leu Arg Ala Leu Arg Asp Leu Thr Arg Val Trp
145             150             155             160

Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Ile Lys Val Leu
            165             170             175

Arg Gly Gln Ile Val Gln Gly Val Ile Trp Leu Leu Leu Val Thr Gly
                180                 185                 190

Ala Gln Gly
        195

<210>   11
<211>   373
<212>   PRT
<213>   Swine fever virus

<400>   11

Arg Leu Ala Cys Lys Glu Asp Tyr Arg Tyr Ala Ile Ser Ser Thr Asn
1               5                   10                  15

Glu Ile Gly Leu Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp Lys Glu
                20                  25                  30

Tyr Asn His Asp Leu Gln Leu Asn Asp Gly Thr Val Lys Ala Ile Cys
            35                  40                  45

Val Ala Gly Ser Phe Lys Val Ile Ala Leu Asn Val Val Ser Arg Arg
        50                  55                  60

Tyr Leu Ala Ser Leu His Lys Glu Ala Ser Leu Thr Ser Val Thr Phe
65                  70                  75                  80

Glu Leu Leu Phe Asp Gly Thr Asn Pro Ser Thr Glu Glu Met Gly Asp
                85                  90                  95

Asp Phe Gly Phe Gly Leu Cys Pro Phe Asp Thr Ser Pro Val Val Lys
            100                 105                 110

Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe Tyr Leu Val
            115                 120                 125

Cys Pro Ile Gly Trp Thr Gly Val Ile Glu Cys Thr Ala Val Ser Pro
    130                 135                 140

Thr Thr Leu Arg Thr Glu Val Val Lys Thr Phe Arg Arg Asp Lys Pro
145                 150                 155                 160

Phe Pro His Arg Met Asp Cys Ala Thr Thr Thr Val Glu Asn Gly Asp
                    165                 170                 175

Leu Phe Tyr Cys Lys Leu Gly Gly Asn Trp Thr Cys Val Lys Gly Glu
                    180                 185                 190

Pro Val Val Tyr Thr Gly Gly Leu Val Lys Gln Cys Arg Trp Cys Gly
                    195                 200                 205

Phe Asp Phe Asn Glu Pro Asp Gly Leu Pro His Tyr Pro Ile Gly Lys
        210                 215                 220

Cys Ile Leu Val Asn Glu Thr Gly Tyr Arg Ile Val Asp Ser Thr Asp
225                 230                 235                 240

Cys Asn Arg Asp Gly Val Val Ile Ser Thr Asp Gly Ser His Glu Cys
                    245                 250                 255

Leu Ile Gly Asn Thr Thr Val Lys Val His Ala Ser Asp Glu Arg Leu
                    260                 265                 270

Gly Pro Met Pro Cys Arg Pro Lys Glu Ile Val Ser Ser Ala Gly Pro
            275                 280                 285

Val Arg Lys Thr Ser Cys Thr Phe Asn Tyr Ala Lys Thr Leu Lys Asn
    290                 295                 300

Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu Lys
305                 310                 315                 320

Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Asp Val Thr Asp Arg His Ser
                    325                 330                 335

Asp Tyr Phe Ala Glu Phe Val Val Leu Val Val Val Ala Leu Leu Gly
            340                 345                 350

Gly Arg Tyr Val Leu Trp Leu Ile Val Thr Tyr Ile Val Leu Thr Glu
            355                 360                 365

Gln Leu Ala Ala Gly
    370

<210> 12

<211> 70
<212> PRT
<213> Swine fever virus

<400> 12

Leu Pro Leu Gly Gln Gly Glu Val Val Leu Ile Gly Asn Leu Ile Thr
1               5                   10                  15

His Thr Asp Ile Glu Val Val Val Tyr Phe Leu Leu Leu Tyr Leu Val
            20                  25                  30

Met Arg Asp Glu Pro Ile Lys Lys Trp Ile Leu Leu Leu Phe His Ala
        35                  40                  45

Met Thr Asn Asn Pro Val Lys Thr Ile Thr Val Ala Leu Leu Met Val
    50                  55                  60

Ser Gly Val Ala Lys Gly
65                  70


<210> 13
<211> 12333
<212> DNA
<213> Border disease virus


<220>
<221> CDS
<222> (877)..(1176)
<223> core protein

<220>
<221> CDS
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                                        Ser Asp Asp Asn Lys Ser
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Glu Lys Thr Asn Glu Lys Lys Pro Asp Arg Val Arg Arg Gly Ala Met
             10              15              20


aag atc aca ccc aaa gag agt gag aag gat agt aga tct aag cca cct      990
Lys Ile Thr Pro Lys Glu Ser Glu Lys Asp Ser Arg Ser Lys Pro Pro
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gac gca act ata gta gta gaa ggc ata aaa tac cag gta aag aag aaa     1038
Asp Ala Thr Ile Val Val Glu Gly Ile Lys Tyr Gln Val Lys Lys Lys
     40              45              50


gga aag gtg aag ggc aag aac aca caa gat ggc tta tac cac aac aag     1086
Gly Lys Val Lys Gly Lys Asn Thr Gln Asp Gly Leu Tyr His Asn Lys
55              60              65                  70


aac aag cca cct gag tct aga aag aaa ttg gag aaa gcc cta ctg gct     1134
Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu Ala
             75              80              85


tgg gct ata ata gca atc ttc atg tgg gaa ccc gta gca cca gag aat     1182
Trp Ala Ile Ile Ala Ile Phe Met Trp Glu Pro Val Ala Pro Glu Asn
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cta atg ttc caa aga ggt gtt aac aga agc ctg cac ggt att tgg cct     1278
Leu Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile Trp Pro
        120                 125                 130

gaa aag ata tgt aca gga gtg ccc acg cac ttg gca aca gat gca gag     1326
Glu Lys Ile Cys Thr Gly Val Pro Thr His Leu Ala Thr Asp Ala Glu
135                 140                 145                 150

ttg aaa gga att caa ggg atg atg gat gct agt gaa aag act aat tac     1374
Leu Lys Gly Ile Gln Gly Met Met Asp Ala Ser Glu Lys Thr Asn Tyr
                155                 160                 165

aca tgc tgc aga ctt cag aga cac gaa tgg aac aag tac ggg tgg tgc     1422
Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys Tyr Gly Trp Cys
                170                 175                 180

aac tgg tac aac ata aat cca tgg ata tgg ttg atg aac aag aca caa     1470
Asn Trp Tyr Asn Ile Asn Pro Trp Ile Trp Leu Met Asn Lys Thr Gln
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gcc aat ctg acg gaa gga cct cca gaa aaa gaa tgc gct gtg acc tgt     1518
Ala Asn Leu Thr Glu Gly Pro Pro Glu Lys Glu Cys Ala Val Thr Cys
200                 205                 210

agg ttc gat aag gaa gca gat ata aat ata gtg aca cag gct agg gac     1566
Arg Phe Asp Lys Glu Ala Asp Ile Asn Ile Val Thr Gln Ala Arg Asp
215                 220                 225                 230

agg cca aca act tta aca ggg tgt aag aaa gga aaa aaa ttt tca ttt     1614
Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Lys Phe Ser Phe
                235                 240                 245

gct ggc atg ata att gag ggc cct tgc aac ttc aat gta tca gtg gaa     1662
Ala Gly Met Ile Ile Glu Gly Pro Cys Asn Phe Asn Val Ser Val Glu
                250                 255                 260

gat ata tta ttc gga gac aat gag tgt agt agc tta ttc cag gac aca     1710
Asp Ile Leu Phe Gly Asp Asn Glu Cys Ser Ser Leu Phe Gln Asp Thr
                265                 270                 275

gct ctc tac gtg gta gat gga gta acc aac acc gta gaa aat gct agg     1758
Ala Leu Tyr Val Val Asp Gly Val Thr Asn Thr Val Glu Asn Ala Arg
        280                 285                 290

caa ggg gct gca aaa ttg aca tcc tgg cta ggg aag caa ttg ggt ata     1806
Gln Gly Ala Ala Lys Leu Thr Ser Trp Leu Gly Lys Gln Leu Gly Ile
295                 300                 305                 310

atg ggg aaa aaa tta gaa cac aag agt aaa acg tgg ttc gga gcc aat     1854
Met Gly Lys Lys Leu Glu His Lys Ser Lys Thr Trp Phe Gly Ala Asn
                315                 320                 325

gca caa tca cct tac tgt aat gta aca aga aaa ata ggg tac gtc tgg     1902
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Ala Gln Ser Pro Tyr Cys Asn Val Thr Arg Lys Ile Gly Tyr Val Trp
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tac aca aac aat tgc acc cct gct tgc ctc cca aag aat aca aaa ata    1950
Tyr Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile
        345             350             355

ata ggt ccg ggg aaa ttt gac acc aat gcg gag gat gga aag atc ttg    1998
Ile Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu
    360             365             370

cat gag atg agg ggt cat ata tcg gaa ttc att cta cta tct ttg gta    2046
His Glu Met Arg Gly His Ile Ser Glu Phe Ile Leu Leu Ser Leu Val
375             380             385             390

gtg cta tca gac ttc gca cct gaa aca gct agt act ctc tac ctg gtg    2094
Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Thr Leu Tyr Leu Val
                395             400             405

cta cat ttt gcc tta cct caa acc cac gaa gtt cct agt gta tgt gac    2142
Leu His Phe Ala Leu Pro Gln Thr His Glu Val Pro Ser Val Cys Asp
                410             415             420

acc aac caa cta aat ctt acg gtc agc ttg aga gtg gat gac gtg ata    2190
Thr Asn Gln Leu Asn Leu Thr Val Ser Leu Arg Val Asp Asp Val Ile
        425             430             435

cca tct tca gta tgg aac ctg gga aaa tat gtc tgt gtt aga cca gac    2238
Pro Ser Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Val Arg Pro Asp
    440             445             450

tgg tgg ccc tat gaa aca acc atg gta ttg ttg ttt gaa gag gca gga    2286
Trp Trp Pro Tyr Glu Thr Thr Met Val Leu Leu Phe Glu Glu Ala Gly
455             460             465             470

caa gta gtg aag ttg gta cta agg gcc ata agg gac ttg aca agg gtc    2334
Gln Val Val Lys Leu Val Leu Arg Ala Ile Arg Asp Leu Thr Arg Val
            475             480             485

tgg aac agt gca tca aca aca gcc ttt ctt ata tgc cta gtt aag gtg    2382
Trp Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Val Lys Val
        490             495             500

tta aga ggc cag gta gta cag gga cta gtg tgg cta tta ctg gta act    2430
Leu Arg Gly Gln Val Val Gln Gly Leu Val Trp Leu Leu Leu Val Thr
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ggt gca caa ggg cag ttt gct tgt aga gaa gac tac agg tat gct tta    2478
Gly Ala Gln Gly Gln Phe Ala Cys Arg Glu Asp Tyr Arg Tyr Ala Leu
    520             525             530

gca aga aca aag gaa ata ggg gcc ctg ggt gca gag agc ttg aca acg    2526
Ala Arg Thr Lys Glu Ile Gly Ala Leu Gly Ala Glu Ser Leu Thr Thr
535             540             545             550

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Thr Trp Thr Asp Tyr Arg Gly Asn Leu Glu Leu Asp Asp Gly Thr Val
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agg gcc aca tgt tcg aga ggt ttc ttt agg ttt aga gga cat tgc atg        2622
Arg Ala Thr Cys Ser Arg Gly Phe Phe Arg Phe Arg Gly His Cys Met
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ata ggg ccc agg tac ctg gct agc cta cac ctg agg gct cta ccc aca        2670
Ile Gly Pro Arg Tyr Leu Ala Ser Leu His Leu Arg Ala Leu Pro Thr
            585             590             595

tct gtc acc ttt gaa cta ata cca gga ggg tca gcg atg aca gaa gag        2718
Ser Val Thr Phe Glu Leu Ile Pro Gly Gly Ser Ala Met Thr Glu Glu
    600             605             610

gaa atg ggt gac gac ttt gaa ttc ggc ctg tgc cct tgt gat tct aga        2766
Glu Met Gly Asp Asp Phe Glu Phe Gly Leu Cys Pro Cys Asp Ser Arg
615             620             625             630

ccc gtt gtt aag gga aaa tac aac acc act ctg ctc aac gga agt gcg        2814
Pro Val Val Lys Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala
            635             640             645

ttc caa cta ata tgc cct tac gga tgg gtc gga cgc gtg gag tgc act        2862
Phe Gln Leu Ile Cys Pro Tyr Gly Trp Val Gly Arg Val Glu Cys Thr
            650             655             660

act gta agc aag agc acc ctg gca aca gag gtg gta aag ata tac aaa        2910
Thr Val Ser Lys Ser Thr Leu Ala Thr Glu Val Val Lys Ile Tyr Lys
            665             670             675

aag aca aaa cca ttt cca cag cgg gtt ggt tgc gac cac acc acc gtc        2958
Lys Thr Lys Pro Phe Pro Gln Arg Val Gly Cys Asp His Thr Thr Val
            680             685             690

tac aaa caa gac ctg tac cat tgc cag atg gga ggt aac tgg acg tgc        3006
Tyr Lys Gln Asp Leu Tyr His Cys Gln Met Gly Gly Asn Trp Thr Cys
695             700             705             710

atg aga ggt gaa gta gtc aaa tat gtg ggg ggt cca gta aag aag tgt        3054
Met Arg Gly Glu Val Val Lys Tyr Val Gly Gly Pro Val Lys Lys Cys
            715             720             725

gag tgg tgc ggc tac gtg ttt aag aag aga gag ggt ctc cca cac tat        3102
Glu Trp Cys Gly Tyr Val Phe Lys Lys Arg Glu Gly Leu Pro His Tyr
            730             735             740

cca att ggt agg tgt atg cta aga aac gag act ggt tac aga agc gtg        3150
Pro Ile Gly Arg Cys Met Leu Arg Asn Glu Thr Gly Tyr Arg Ser Val
            745             750             755

gat gac aca cca tgc gat aga ggt gga gtc gtg atc agc aaa acc ggt        3198
Asp Asp Thr Pro Cys Asp Arg Gly Gly Val Val Ile Ser Lys Thr Gly
            760             765             770

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Glu Leu Glu Cys Leu Ile Gly Lys Thr Thr Val Lys Val Phe Ser Ser
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agt gaa gga ccg gtc agc aag ata gct tgc aca ttc aac tac tca aaa          3342
Ser Glu Gly Pro Val Ser Lys Ile Ala Cys Thr Phe Asn Tyr Ser Lys
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acc ctg gaa aac aaa tac tat gag ccc aga gac agt tat ttc cag caa          3390
Thr Leu Glu Asn Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln
            825             830             835

tac atg ctc aag gga caa tac caa tac tgg ttc gat ctt gaa gca aca          3438
Tyr Met Leu Lys Gly Gln Tyr Gln Tyr Trp Phe Asp Leu Glu Ala Thr
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Asp His His Ser Asp Tyr Phe Ala Glu Phe Ile Met Leu Ala Val Val
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gcc ctg cta ggg ggg agg tat gtc tta tgg tta atg gtt gtc tac atg          3534
Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Met Val Val Tyr Met
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atc ctg gca gat caa atg acc tca gca ata aac ctg ggc caa gga gag          3582
Ile Leu Ala Asp Gln Met Thr Ser Ala Ile Asn Leu Gly Gln Gly Glu
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Val Val Leu Ile Gly Asn Leu Ile Thr His Glu Asp His Glu Val Val
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gta tat ttc ctc ctg tta tac tta ata gtg aag gat gag cca gta aag          3678
Val Tyr Phe Leu Leu Leu Tyr Leu Ile Val Lys Asp Glu Pro Val Lys
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aag tgg ata ttg ttc ctc ttt cat gct atg acc aac aac cct gta aag          3726
Lys Trp Ile Leu Phe Leu Phe His Ala Met Thr Asn Asn Pro Val Lys
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gaatatgtag attacaaagg cactttccta acaagagaga ccctggaagc acttagtctg   9651

ggtaagccaa aagccaaaaa tataaccaaa gctgatgctc acaggctact caacccagaa   9711

aaagagcaga ttggattacc tgactggttc acagctacgg aacctatatt cctggaagct   9771

atgataaaac aagaaaaata ccacataaca ggggatgtag caaccgtgaa agacaaagcc   9831

aaacaattag gggccaccga ttccacgaga atagttaagg aggtaggtgc cagggtgtac   9891

accatgaagc ttaatagctg ggctttgcaa gctgaaagag gggatgcaaa cctcaaaccc   9951

ttatttgaag aacttctgct acagtgccca cccgggagaa cagtcaaagg cggaaccatg   10011

gtgtcggcat accagcttgc acaggggaac tggacgccaa ctagctgtaa agtatacatg   10071

gggactataa cagcaaaaag agtaaaaata cacccatatg aagcatatat aaaattgaag   10131

gagcttatag aagagtacaa catgaaaagg gtgactggag atacaggtct aaagagacat   10191

aatgaatgga tcttaaagag aatcaaacac cacgggaacc tgaggactaa gaaaatactg   10251

aacccaggta agtagcaga acaactcagc agagaaggtc ataaacacaa tgtgtacaac   10311

aagataatag gttcaactat ggcatcagtg ggaatcaagc tggagaagct accagtagtg   10371

agggctcaaa cggacacaac cttttttccat caagccatta gggataaaat agacaaagaa   10431

gagaacccgc agacaccaga cctgcataag gaattgaaag aagttttcaa tgccctaaaa   10491

ataccagaac tcgctgctac ttatgatgca gttgaatggg aggaactgga gacaggtatc   10551

aacaggaaag gagcagctgg ttttttttgaa aggaaaaaca ttggtgaaat actggataca   10611

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gattttgtag atgaaaagaa accgagagtg atacagtacc cagaggccaa agtcaggcta   10791

gctataacga aggtcatgta caagtgggtc aaacaaaaac cagtggtcat tcccgggtat   10851

gaaggtaaga caccattgtt tgagatattt gataaggtaa aaaaagaatg gggtagcttc   10911

gataatccag ttgcagtgag ctttgacact aaggcttggg acacacaagt taccagcaaa   10971
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agcctagagc tgattaggga catacagaaa tactatttca agaaggagtg gcataaattc  11031

attgagacta taactgagca catggtagaa gtgccggtag tcacagctga tggggaggtg  11091

tacatcagcg agggccaaag aggtagtggt caaccggaca ctagtgctgg caatagtatg  11151

ttaaatgtct taaccatggt ttatgctttc tgccgagcca caggcgtgcc ctacaaaagt  11211

ttcaaaaggg ttgccaagat acatgtctgt ggagatgatg gcttttttgat aacggagaaa  11271

agcctaggag agaaatttgc cagtaagggt atacaaatcc tacatgaagc aggaaaaccc  11331

cagaaaatta cagagggga ccgcatgaaa gtagcttata agtttgagga catagaattt  11391

tgctctcaca cccctgtgcc tgtgaggtgg tcagacaaca ccactagcta tatgccaggt  11451

aggaacaccg cgactatcct ggctaagatg gccacaaggc tagattcaag tggagaaagg  11511

gggacaacag catatgagaa ggcagtggct tttagttttc tcctgatgta ctcatggaac  11571

cctctggtta gaaggatttg cctacttacg ctatcgagcg agttgggcac caaacctagt  11631

aaacggacca cctattacta cgaaggcgat ccaatatctg cctataggga ggtgattggc  11691

cacaacttac tagacctgaa gaggacaggc ttggagaaac tggcactatt aaacctgagt  11751

atgtctactc taggtatatg gacaaaacac atcagtaaaa ggttgctaca agactgcgtt  11811

gatgtaggca gcaaggatgg caattggctg gtaaacgcag ataggccgga gagcagaaaa  11871

acaggaaagg tctacttgca aagtggaggc cataccgtaa gagggaggca ttatgaagac  11931

ctgatattgc ctaggatggt gaaaccaaca tttcaaggag tagacagata caaattggga  11991

cccatagtca acgtaatatt cagaaggctg agggttatga tgatggccct ggttggtaga  12051

gggatgtgaa ccatagctga gcatttcatg acaacacgcc aagggccact aaattgtata  12111

tataactgtg taaatattta cctatttatt tactgttatt tatttaatag agacagtgat  12171

atttatttaa tagcttatct atttatttat ttgatgggat gtagatggca actaactacc  12231

tcataggacc acactacact cattttaaa actacagcac tttagctgga agggaaaagc  12291

ctgaagtcca gagttggatt aaggaaaaac cctaacagcc cc                      12333
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<210> 14
<211> 100
<212> PRT
<213> Border disease virus

<400> 14

Ser Asp Asp Asn Lys Ser Glu Lys Thr Asn Glu Lys Lys Pro Asp Arg
1   5   10   15

Val Arg Arg Gly Ala Met Lys Ile Thr Pro Lys Glu Ser Glu Lys Asp
        20   25   30

Ser Arg Ser Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly Ile Lys
        35   40   45

Tyr Gln Val Lys Lys Lys Gly Lys Val Lys Gly Lys Asn Thr Gln Asp
    50   55   60

Gly Leu Tyr His Asn Lys Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu
65   70   75   80

Glu Lys Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Phe Met Trp Glu
            85   90   95

Pro Val Ala Pro
            100

<210> 15
<211> 227
<212> PRT
<213> Border disease virus

<400> 15

Glu Asn Val Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Thr Gly Ile
1   5   10   15

Gln Leu Leu Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile
            20   25   30

Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Thr His Leu Ala Thr Asp
        35   40   45

Ala Glu Leu Lys Gly Ile Gln Gly Met Met Asp Ala Ser Glu Lys Thr
    50   55   60

Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys Tyr Gly
65   70   75   80

Trp Cys Asn Trp Tyr Asn Ile Asn Pro Trp Ile Trp Leu Met Asn Lys
            85   90   95

Thr Gln Ala Asn Leu Thr Glu Gly Pro Pro Glu Lys Glu Cys Ala Val

Thr Cys Arg Phe Asp Lys Glu Ala Asp Ile Asn Ile Val Thr Gln Ala
        115   120   125

Arg Asp Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Lys Phe
    130   135   140

Ser Phe Ala Gly Met Ile Ile Glu Gly Pro Cys Asn Phe Asn Val Ser
145   150   155   160

Val Glu Asp Ile Leu Phe Gly Asp Asn Glu Cys Ser Ser Leu Phe Gln
                165   170   175

Asp Thr Ala Leu Tyr Val Val Asp Gly Val Thr Asn Thr Val Glu Asn
            180   185   190

Ala Arg Gln Gly Ala Ala Lys Leu Thr Ser Trp Leu Gly Lys Gln Leu
        195   200   205

Gly Ile Met Gly Lys Lys Leu Glu His Lys Ser Lys Thr Trp Phe Gly
    210   215   220

Ala Asn Ala
225

<210>   16
<211>   195
<212>   PRT
<213>   Border disease virus

<400>   16

Gln Ser Pro Tyr Cys Asn Val Thr Arg Lys Ile Gly Tyr Val Trp Tyr
1   5   10   15

Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile
            20   25   30

Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His
        35   40   45

Glu Met Arg Gly His Ile Ser Glu Phe Ile Leu Leu Ser Leu Val Val
    50   55   60

```
Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Thr Leu Tyr Leu Val Leu
65              70              75              80

His Phe Ala Leu Pro Gln Thr His Glu Val Pro Ser Val Cys Asp Thr
                85              90              95

Asn Gln Leu Asn Leu Thr Val Ser Leu Arg Val Asp Asp Val Ile Pro
            100             105             110

Ser Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Val Arg Pro Asp Trp
        115             120             125

Trp Pro Tyr Glu Thr Thr Met Val Leu Leu Phe Glu Glu Ala Gly Gln
    130             135             140

Val Val Lys Leu Val Leu Arg Ala Ile Arg Asp Leu Thr Arg Val Trp
145             150             155             160

Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Val Lys Val Leu
            165             170             175

Arg Gly Gln Val Val Gln Gly Leu Val Trp Leu Leu Leu Val Thr Gly
        180             185             190

Ala Gln Gly
        195


<210>   17
<211>   373
<212>   PRT
<213>   Border disease virus

<400>   17

Gln Phe Ala Cys Arg Glu Asp Tyr Arg Tyr Ala Leu Ala Arg Thr Lys
1               5               10              15

Glu Ile Gly Ala Leu Gly Ala Glu Ser Leu Thr Thr Thr Trp Thr Asp
            20              25              30

Tyr Arg Gly Asn Leu Glu Leu Asp Asp Gly Thr Val Arg Ala Thr Cys
        35              40              45

Ser Arg Gly Phe Phe Arg Phe Arg Gly His Cys Met Ile Gly Pro Arg
```

Tyr Leu Ala Ser Leu His Leu Arg Ala Leu Pro Thr Ser Val Thr Phe
65   70   75   80

Glu Leu Ile Pro Gly Gly Ser Ala Met Thr Glu Glu Glu Met Gly Asp
                85   90   95

Asp Phe Glu Phe Gly Leu Cys Pro Cys Asp Ser Arg Pro Val Val Lys
            100   105   110

Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe Gln Leu Ile
        115   120   125

Cys Pro Tyr Gly Trp Val Gly Arg Val Glu Cys Thr Thr Val Ser Lys
    130   135   140

Ser Thr Leu Ala Thr Glu Val Val Lys Ile Tyr Lys Lys Thr Lys Pro
145   150   155   160

Phe Pro Gln Arg Val Gly Cys Asp His Thr Thr Val Tyr Lys Gln Asp
            165   170   175

Leu Tyr His Cys Gln Met Gly Gly Asn Trp Thr Cys Met Arg Gly Glu
        180   185   190

Val Val Lys Tyr Val Gly Gly Pro Val Lys Lys Cys Glu Trp Cys Gly
    195   200   205

Tyr Val Phe Lys Lys Arg Glu Gly Leu Pro His Tyr Pro Ile Gly Arg
    210   215   220

Cys Met Leu Arg Asn Glu Thr Gly Tyr Arg Ser Val Asp Asp Thr Pro
225   230   235   240

Cys Asp Arg Gly Gly Val Val Ile Ser Lys Thr Gly Glu Leu Glu Cys
            245   250   255

Leu Ile Gly Lys Thr Thr Val Lys Val Phe Ser Ser Asp Lys Lys Leu
            260   265   270

Gly Pro Met Pro Cys Arg Pro Lys Glu Val Ile Ser Ser Glu Gly Pro
        275   280   285

Val Ser Lys Ile Ala Cys Thr Phe Asn Tyr Ser Lys Thr Leu Glu Asn
    290   295   300

Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu Lys
305   310   315   320

Gly Gln Tyr Gln Tyr Trp Phe Asp Leu Glu Ala Thr Asp His His Ser
                325   330   335

Asp Tyr Phe Ala Glu Phe Ile Met Leu Ala Val Val Ala Leu Leu Gly
            340   345   350

Gly Arg Tyr Val Leu Trp Leu Met Val Val Tyr Met Ile Leu Ala Asp
        355   360   365

Gln Met Thr Ser Ala
    370

<210> 18
<211> 70
<212> PRT
<213> Border disease virus

<400> 18

Ile Asn Leu Gly Gln Gly Glu Val Val Leu Ile Gly Asn Leu Ile Thr
1   5   10   15

His Glu Asp His Glu Val Val Val Tyr Phe Leu Leu Leu Tyr Leu Ile
                20   25   30

Val Lys Asp Glu Pro Val Lys Lys Trp Ile Leu Phe Leu Phe His Ala
            35   40   45

Met Thr Asn Asn Pro Val Lys Thr Ile Ser Val Gly Leu Leu Met Leu
    50   55   60

Ser Gly Leu Val Lys Gly
65   70

<210> 19
<211> 2694
<212> DNA
<213> Bovine viral diarrhea virus : deltaCErnsE1E2p7

<400> 19
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atagctatag ttttgtttca agttacaatg ggagaaaaca taacacagtg gaacctacaa   120

gataatggga cggaagggat acaacgggca atgttccaaa ggggtgtgaa tagaagttta   180

catggaatct ggccagagaa aatctgtact ggcgtccctt cccatctagc caccgatata   240

gaactaaaaa caattcatgg tatgatggat gcaagtgaga agaccaacta cacgtgttgc   300

agacttcaac gccatgagtg gaacaagcat ggttggtgca actggtacaa tattgaaccc   360

tggattctag tcatgaatag aacccaagcc aatctcactg agggacaacc accaagggag   420

tgcgcagtca cttgtaggta tgatagggct agtgacttaa cgtggtaac acaagctaga   480

gatagcccca caccttaac aggttgcaag aaaggaaaga acttctcctt tgcaggcata   540

ttgatgcggg cccctgcaa ctttgaaata gctgcaagtg atgtattatt caaagaacat   600

gaacgcatta gtatgttcca ggataccact ctttaccttg ttgacgggtt gaccaactcc   660

ttagaaggtg ccagacaagg aaccgctaaa ctgacaacct ggttaggcaa gcagctcggg   720

atactaggaa aaagttgga aaacaagagt aagacgtggt ttggagcata cgctgcttcc   780

ccttactgtg atgtcgatcg caaaattggc tacatatggt atacaaaaaa ttgcaccct   840

gcctgcttac ccaagaacac aaaaattgtc ggccctggga aatttggcac caatgcagag   900

gacggcaaga tattacatga gatggggggt cacttgtcgg aggtactact actttctta   960

gtggtgctgt ccgacttcgc accggaaaca gctagtgtaa tgtacctaat cctacatttt   1020

tccatcccac aaagtcacgt tgatgtaatg gattgtgata gacccagtt gaacctcaca   1080

gtggagctga caacagctga agtaatacca gggtcggtct ggaatctagg caaatatgta   1140

tgtataagac caaattggtg gccttatgag acaactgtag tgttggcatt tgaagaggtg   1200

agccaggtgg tgaagttagt gttgagggca ctcagagatt aacacgcat ttggaacgct   1260

gcaacaacta ctgctttttt agtatgcctt gttaagatag tcaggggcca gatggtacag   1320

ggcattctgt ggctactatt gataacaggg gtacaagggc acttggattg caaacctgaa   1380

ttctcgtatg ccatagcaaa ggacgaaaga attggtcaac tgggggctga aggccttacc   1440

accacttgga aggaatactc acctggaatg aagctggaag acacaatggt cattgcttgg   1500

tgcgaagatg ggaagttaat gtacctccaa agatgcacga gagaaaccag atatctcgca   1560

atcttgcata caagagcctt gccgaccagt gtggtattca aaaaactctt tgatgggcga   1620

aagcaagagg atgtagtcga aatgaacgac aactttgaat ttggactctg cccatgtgat   1680

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gccaaaccca tagtaagagg gaagttcaat acaacgctgc tgaacggacc ggccttccag    1740

atggtatgcc ccataggatg gacagggact gtaagctgta cgtcattcaa tatggacacc    1800

ttagccacaa ctgtggtacg gacatataga aggtctaaac cattccctca taggcaaggc    1860

tgtatcaccc aaaagaatct gggggaggat ctccataact gcatccttgg aggaaattgg    1920

acttgtgtgc ctggagacca actactatac aaagggggct ctattgaatc ttgcaagtgg    1980

tgtggctatc aatttaaaga gagtgaggga ctaccacact accccattgg caagtgtaaa    2040

ttggagaacg agactggtta caggctagta gacagtacct cttgcaatag agaaggtgtg    2100

gccatagtac cacaagggac attaaagtgc aagataggaa aaacaactgt acaggtcata    2160

gctatggata ccaaactcgg acctatgcct tgcagaccat atgaaatcat atcaagtgag    2220

gggcctgtag aaaagacagc gtgtactttc aactacacta agacattaaa aaataagtat    2280

tttgagccca gagacagcta ctttcagcaa tacatgctaa aaggagagta tcaatactgg    2340

tttgacctgg aggtgactga ccatcaccgg gattacttcg ctgagtccat attagtggtg    2400

gtagtagccc tcttgggtgg cagatatgta ctttggttac tggttacata catggtctta    2460

tcagaacaga aggccttagg gattcagtat ggatcagggg aagtggtgat gatgggcaac    2520

ttgctaaccc ataacaatat tgaagtggtg acatacttct tgctgctgta cctactgctg    2580

agggaggaga gcgtaaagaa gtgggtctta ctcttatacc acatcttagt ggtacaccca    2640

atcaaatctg taattgtgat cctactgatg attggggatg tggtaaaggc ctga          2694
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<210> 20
<211> 900
<212> PRT
<213> Bovine viral diarrhea virus : deltaCErnsE1E2p7

<220>
<221> MISC_FEATURE
<222> (1)..(34)
<223> core protein

<220>
<221> MISC_FEATURE
<222> (35)..(261)
<223> Erns

<220>
<221> MISC_FEATURE
<222> (262)..(456)
<223> E1

<220>
<221> MISC_FEATURE
<222> (457)..(456)
<223> E1

<220>
<221> MISC_FEATURE
<222> (457)..(830)
<223> E2

<220>
<221> MISC_FEATURE
<222> (831)..(900)
<223> p7

<400> 20

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Met Asn Ser Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys
1               5                   10                  15


Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr
                20                  25                  30


Met Gly Glu Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu
            35                  40                  45


Gly Ile Gln Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His
        50                  55                  60


Gly Ile Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala
65                  70                  75                  80


Thr Asp Ile Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu
                85                  90                  95


Lys Thr Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys
            100                 105                 110


His Gly Trp Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met
            115                 120                 125


Asn Arg Thr Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys
        130                 135                 140


Ala Val Thr Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val Thr
145                 150                 155                 160
```

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Gln Ala Arg Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys
              165              170              175


Asn Phe Ser Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe Glu
              180              185              190


Ile Ala Ala Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser Met
              195              200              205


Phe Gln Asp Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser Leu
      210              215              220


Glu Gly Ala Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly Lys
225                   230              235              240


Gln Leu Gly Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr Trp
              245              250              255


Phe Gly Ala Tyr Ala Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile
              260              265              270


Gly Tyr Ile Trp Tyr Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys
              275              280              285


Asn Thr Lys Ile Val Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp
      290              295              300


Gly Lys Ile Leu His Glu Met Gly Gly His Leu Ser Glu Val Leu Leu
305              310              315              320


Leu Ser Leu Val Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Val
              325              330              335


Met Tyr Leu Ile Leu His Phe Ser Ile Pro Gln Ser His Val Asp Val
              340              345              350


Met Asp Cys Asp Lys Thr Gln Leu Asn Leu Thr Val Glu Leu Thr Thr
      355              360              365


Ala Glu Val Ile Pro Gly Ser Val Trp Asn Leu Gly Lys Tyr Val Cys
      370              375              380


Ile Arg Pro Asn Trp Trp Pro Tyr Glu Thr Thr Val Val Leu Ala Phe
```

385   390   395   400

Glu Glu Val Ser Gln Val Val Lys Leu Val Leu Arg Ala Leu Arg Asp
              405   410   415

Leu Thr Arg Ile Trp Asn Ala Ala Thr Thr Ala Phe Leu Val Cys
              420   425   430

Leu Val Lys Ile Val Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu
              435   440   445

Leu Leu Ile Thr Gly Val Gln Gly His Leu Asp Cys Lys Pro Glu Phe
         450   455   460

Ser Tyr Ala Ile Ala Lys Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu
465   470   475   480

Gly Leu Thr Thr Thr Trp Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu
              485   490   495

Asp Thr Met Val Ile Ala Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu
              500   505   510

Gln Arg Cys Thr Arg Glu Thr Arg Tyr Leu Ala Ile Leu His Thr Arg
         515   520   525

Ala Leu Pro Thr Ser Val Val Phe Lys Lys Leu Phe Asp Gly Arg Lys
         530   535   540

Gln Glu Asp Val Val Glu Met Asn Asp Asn Phe Glu Phe Gly Leu Cys
545   550   555   560

Pro Cys Asp Ala Lys Pro Ile Val Arg Gly Lys Phe Asn Thr Thr Leu
              565   570   575

Leu Asn Gly Pro Ala Phe Gln Met Val Cys Pro Ile Gly Trp Thr Gly
              580   585   590

Thr Val Ser Cys Thr Ser Phe Asn Met Asp Thr Leu Ala Thr Thr Val
              595   600   605

Val Arg Thr Tyr Arg Arg Ser Lys Pro Phe Pro His Arg Gln Gly Cys
         610   615   620

Ile Thr Gln Lys Asn Leu Gly Glu Asp Leu His Asn Cys Ile Leu Gly
625   630   635   640

Gly Asn Trp Thr Cys Val Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly
            645   650   655

Ser Ile Glu Ser Cys Lys Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu
            660   665   670

Gly Leu Pro His Tyr Pro Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr
            675   680   685

Gly Tyr Arg Leu Val Asp Ser Thr Ser Cys Asn Arg Glu Gly Val Ala
            690   695   700

Ile Val Pro Gln Gly Thr Leu Lys Cys Lys Ile Gly Lys Thr Thr Val
705   710   715   720

Gln Val Ile Ala Met Asp Thr Lys Leu Gly Pro Met Pro Cys Arg Pro
                725   730   735

Tyr Glu Ile Ile Ser Ser Glu Gly Pro Val Glu Lys Thr Ala Cys Thr
            740   745   750

Phe Asn Tyr Thr Lys Thr Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp
            755   760   765

Ser Tyr Phe Gln Gln Tyr Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe
            770   775   780

Asp Leu Glu Val Thr Asp His His Arg Asp Tyr Phe Ala Glu Ser Ile
785   790   795   800

Leu Val Val Val Val Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu
                805   810   815

Leu Val Thr Tyr Met Val Leu Ser Glu Gln Lys Ala Leu Gly Ile Gln
            820   825   830

Tyr Gly Ser Gly Glu Val Val Met Met Gly Asn Leu Leu Thr His Asn
            835   840   845

Asn Ile Glu Val Val Thr Tyr Phe Leu Leu Leu Tyr Leu Leu Leu Arg
    850   855   860

Glu Glu Ser Val Lys Lys Trp Val Leu Leu Leu Tyr His Ile Leu Val
865   870   875   880

Val His Pro Ile Lys Ser Val Ile Val Ile Leu Leu Met Ile Gly Asp
              885   890   895

Val Val Lys Ala
          900

<210> 21
<211> 2484
<212> DNA
<213> Bovine viral diarrhea virus : delraCErnsE1E2

<400> 21
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gataatggga cggaagggat acaacgggca atgttccaaa ggggtgtgaa tagaagttta   180

catggaatct ggccagagaa aatctgtact ggcgtccctt cccatctagc caccgatata   240

gaactaaaaa caattcatgg tatgatggat gcaagtgaga agaccaacta cacgtgttgc   300

agacttcaac gccatgagtg gaacaagcat ggttggtgca actggtacaa tattgaaccc   360

tggattctag tcatgaatag aacccaagcc aatctcactg agggacaacc accaagggag   420

tgcgcagtca cttgtaggta tgatagggct agtgacttaa acgtggtaac acaagctaga   480

gatagcccca caccottaac aggttgcaag aaaggaaaga acttctcctt tgcaggcata   540

ttgatgcggg gcccctgcaa ctttgaaata gctgcaagtg atgtattatt caaagaacat   600

gaacgcatta gtatgttcca ggataccact ctttaccttg ttgacgggtt gaccaactcc   660

ttagaaggtg ccagacaagg aaccgctaaa ctgacaacct ggttaggcaa gcagctcggg   720

atactaggaa aaaagttgga aaacaagagt aagacgtggt ttggagcata cgctgcttcc   780

ccttactgtg atgtcgatcg caaaattggc tacatatggt atacaaaaaa ttgcacccct   840

gcctgcttac ccaagaacac aaaaattgtc ggccctggga aatttggcac caatgcagag   900

gacggcaaga tattacatga gatggggggt cacttgtcgg aggtactact actttctttа   960

gtggtgctgt ccgacttcgc accggaaaca gctagtgtaa tgtacctaat cctacatttt   1020

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tccatcccac aaagtcacgt tgatgtaatg gattgtgata agacccagtt gaacctcaca      1080

gtggagctga caacagctga agtaatacca gggtcggtct ggaatctagg caaatatgta      1140

tgtataagac caaattggtg gccttatgag acaactgtag tgttggcatt tgaagaggtg      1200

agccaggtgg tgaagttagt gttgagggca ctcagagatt taacacgcat ttggaacgct      1260

gcaacaacta ctgctttttt agtatgcctt gttaagatag tcaggggcca gatggtacag      1320

ggcattctgt ggctactatt gataacaggg gtacaagggc acttggattg caaacctgaa      1380

ttctcgtatg ccatagcaaa ggacgaaaga attggtcaac tgggggctga aggccttacc      1440

accacttgga aggaatactc acctggaatg aagctggaag acacaatggt cattgcttgg      1500

tgcgaagatg ggaagttaat gtacctccaa agatgcacga gagaaaccag atatctcgca      1560

atcttgcata aagagcctt gccgaccagt gtggtattca aaaaactctt tgatgggcga      1620

aagcaagagg atgtagtcga aatgaacgac aactttgaat ttggactctg cccatgtgat      1680

gccaaaccca tagtaagagg gaagttcaat acaacgctgc tgaacggacc ggccttccag      1740

atggtatgcc ccataggatg acagggact gtaagctgta cgtcattcaa tatggacacc      1800

ttagccacaa ctgtggtacg gacatataga aggtctaaac cattccctca taggcaaggc      1860

tgtatcaccc aaaagaatct ggggggaggat ctccataact gcatccttgg aggaaattgg      1920

acttgtgtgc ctggagacca actactatac aaaggggggct ctattgaatc ttgcaagtgg      1980

tgtggctatc aatttaaaga gagtgaggga ctaccacact accccattgg caagtgtaaa      2040

ttggagaacg agactggtta caggctagta gacagtacct cttgcaatag agaaggtgtg      2100

gccatagtac cacaagggac attaaagtgc aagataggaa aaacaactgt acaggtcata      2160

gctatggata ccaaactcgg acctatgcct tgcagaccat atgaaatcat atcaagtgag      2220

gggcctgtag aaaagacagc gtgtactttc aactacacta agacattaaa aaataagtat      2280

tttgagccca gagacagcta ctttcagcaa tacatgctaa aaggagagta tcaatactgg      2340

tttgacctgg aggtgactga ccatcaccgg gattacttcg ctgagtccat attagtggtg      2400

gtagtagccc tcttgggtgg cagatatgta ctttggttac tggttacata catggtctta      2460

tcagaacaga aggccttagg gtga                                              2484


<210>  22
<211>  827
<212>  PRT
<213>  Bovine viral diarrhea virus : deltaCErnsE1E2

<400>  22
```

```
Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
1           5               10              15

Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Glu
        20              25              30

Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu Gly Ile Gln
        35              40              45

Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile Trp
    50              55              60

Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala Thr Asp Ile
65              70              75              80

Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu Lys Thr Asn
                85              90              95

Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys His Gly Trp
            100             105             110

Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met Asn Arg Thr
        115             120             125

Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys Ala Val Thr
    130             135             140

Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val Thr Gln Ala Arg
145             150             155             160

Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe Ser
            165             170             175

Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe Glu Ile Ala Ala
        180             185             190

Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser Met Phe Gln Asp
        195             200             205

Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser Leu Glu Gly Ala
    210             215             220
```

```
Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly Lys Gln Leu Gly
225             230             235             240


Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr Trp Phe Gly Ala
            245             250             255


Tyr Ala Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile
            260             265             270


Trp Tyr Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys
        275             280             285


Ile Val Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile
    290             295             300


Leu His Glu Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu
305             310             315             320


Val Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu
            325             330             335


Ile Leu His Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys
            340             345             350


Asp Lys Thr Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val
        355             360             365


Ile Pro Gly Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro
    370             375             380


Asn Trp Trp Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val
385             390             395             400


Ser Gln Val Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg
            405             410             415


Ile Trp Asn Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys
            420             425             430


Ile Val Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile
            435             440             445


Thr Gly Val Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala
```

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                450                   455                   460


Ile Ala Lys Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr
465                 470                 475                 480


Thr Thr Trp Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met
                485                 490                 495


Val Ile Ala Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys
            500                 505                 510


Thr Arg Glu Thr Arg Tyr Leu Ala Ile Leu His`Thr Arg Ala Leu Pro
        515                 520                 525


Thr Ser Val Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp
        530                 535                 540


Val Val Glu Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp
545                 550                 555                 560


Ala Lys Pro Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly
                565                 570                 575


Pro Ala Phe Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser
            580                 585                 590


Cys Thr Ser Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr
        595                 600                 605


Tyr Arg Arg Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln
    610                 615                 620


Lys Asn Leu Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp
625                 630                 635                 640


Thr Cys Val Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu
                645                 650                 655


Ser Cys Lys Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro
            660                 665                 670


His Tyr Pro Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg
    675                 680                 685
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Leu Val Asp Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro
    690                 695                 700

Gln Gly Thr Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile
705                 710                 715                 720

Ala Met Asp Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile
                725                 730                 735

Ile Ser Ser Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr
                740                 745                 750

Thr Lys Thr Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe
                755                 760                 765

Gln Gln Tyr Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu
    770                 775                 780

Val Thr Asp His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val
785                 790                 795                 800

Val Val Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr
                805                 810                 815

Tyr Met Val Leu Ser Glu Gln Lys Ala Leu Gly
            820                 825


<210>  23
<211>  2013
<212>  DNA
<213>  Bovine viral diarrhea virus : deltaCE1E2p7

<400>  23
aaaaacaaac ctcaggaatc acgcaagaaa ctggaaaaag cattgttggc gtgggcaata      60

atagctatag ttttgtttca agttacaatg ggagcttccc cttactgtga tgtcgatcgc     120

aaaattggct acatatggta tacaaaaaat tgcacccctg cctgcttacc caagaacaca     180

aaaattgtcg gccctgggaa atttggcacc aatgcagagg acggcaagat attacatgag     240

atggggggtc acttgtcgga ggtactacta ctttctttag tggtgctgtc cgacttcgca     300

ccggaaacag ctagtgtaat gtacctaatc ctacattttt ccatcccaca aagtcacgtt     360

gatgtaatgg attgtgataa gacccagttg aacctcacag tggagctgac aacagctgaa     420
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gtaataccag ggtcggtctg gaatctaggc aaatatgtat gtataagacc aaattggtgg   480

ccttatgaga caactgtagt gttggcattt gaagaggtga gccaggtggt gaagttagtg   540

ttgagggcac tcagagattt aacacgcatt tggaacgctg caacaactac tgcttttta   600

gtatgccttg ttaagatagt caggggccag atggtacagg gcattctgtg gctactattg   660

ataacagggg tacaagggca cttggattgc aaacctgaat tctcgtatgc catagcaaag   720

gacgaaagaa ttggtcaact gggggctgaa ggccttacca ccacttggaa ggaatactca   780

cctggaatga agctggaaga cacaatggtc attgcttggt gcgaagatgg gaagttaatg   840

tacctccaaa gatgcacgag agaaaccaga tatctcgcaa tcttgcatac aagagccttg   900

ccgaccagtg tggtattcaa aaaactcttt gatgggcgaa agcaagagga tgtagtcgaa   960

atgaacgaca actttgaatt tggactctgc ccatgtgatg ccaaacccat agtaagaggg   1020

aagttcaata caacgctgct gaacggaccg gccttccaga tggtatgccc cataggatgg   1080

acagggactg taagctgtac gtcattcaat atggacacct agccacaac tgtggtacgg   1140

acatatagaa ggtctaaacc attccctcat aggcaaggct gtatcaccca aaagaatctg   1200

ggggaggatc tccataactg catccttgga ggaaattgga cttgtgtgcc tggagaccaa   1260

ctactataca aaggggctc tattgaatct tgcaagtggt gtggctatca atttaaagag   1320

agtgagggac taccacacta ccccattggc aagtgtaaat tggagaacga gactggttac   1380

aggctagtag acagtacctc ttgcaataga gaaggtgtgg ccatagtacc acaagggaca   1440

ttaaagtgca agataggaaa aacaactgta caggtcatag ctatggatac aaaactcgga   1500

cctatgcctt gcagaccata tgaaatcata tcaagtgagg ggcctgtaga aaagacagcg   1560

tgtactttca actacactaa gacattaaaa aataagtatt ttgagcccag agacagctac   1620

tttcagcaat acatgctaaa aggagagtat caatactggt ttgacctgga ggtgactgac   1680

catcaccggg attacttcgc tgagtccata ttagtggtgg tagtagccct cttgggtggc   1740

agatatgtac tttggttact ggttacatac atggtcttat cagaacagaa ggccttaggg   1800

attcagtatg gatcagggga agtggtgatg atgggcaact gctaaccca taacaatatt   1860

gaagtggtga catacttctt gctgctgtac ctactgctga gggaggagag cgtaaagaag   1920

tgggtcttac tcttatacca catcttagtg gtacacccaa tcaaatctgt aattgtgatc   1980

ctactgatga ttggggatgt ggtaaaggcc tga   2013

<210> 24

<211> 670
<212> PRT
<213> Bovine viral diarrhea virus : deltaCE1E2p7

<400> 24

Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
1   5   10   15

Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Ala
                20   25   30

Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr Thr
        35   40   45

Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val Gly
    50   55   60

Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His Glu
65   70   75   80

Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val Leu
                85   90   95

Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu His
            100   105   110

Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys Thr
            115   120   125

Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro Gly
    130   135   140

Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp Trp
145   150   155   160

Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln Val
                165   170   175

Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp Asn
            180   185   190

Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val Arg
            195   200   205

```
Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly Val
    210             215                 220

Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys
225                 230                 235                 240

Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp
                245                 250                 255

Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala
                260                 265                 270

Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu
        275                 280                 285

Thr Arg Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val
    290                 295                 300

Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu
305                 310                 315                 320

Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro
                325                 330                 335

Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe
                340                 345                 350

Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser
        355                 360                 365

Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg
    370                 375                 380

Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu
385                 390                 395                 400

Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val
                405                 410                 415

Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys
                420                 425                 430
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Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro
    435                 440             445

Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp
    450                 455             460

Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr
465                 470             475             480

Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp
            485             490             495

Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser
            500             505             510

Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr
            515             520             525

Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr
    530             535             540

Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp
545             550             555             560

His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala
            565             570             575

Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val
            580             585             590

Leu Ser Glu Gln Lys Ala Leu Gly Ile Gln Tyr Gly Ser Gly Glu Val
    595             600             605

Val Met Met Gly Asn Leu Leu Thr His Asn Asn Ile Glu Val Val Thr
    610             615             620

Tyr Phe Leu Leu Leu Tyr Leu Leu Leu Arg Glu Glu Ser Val Lys Lys
625             630             635             640

Trp Val Leu Leu Leu·Tyr His Ile Leu Val Val His Pro Ile Lys Ser
            645             650             655

Val Ile Val Ile Leu Leu Met Ile Gly Asp Val Val Lys Ala
```

<210> 25
<211> 1803
<212> DNA
<213> Bovine viral diarrhea virus : deltaCE1E2

<400> 25
aaaaacaaac ctcaggaatc acgcaagaaa ctggaaaaag cattgttggc gtgggcaata   60

atagctatag ttttgtttca agttacaatg ggagcttccc cttactgtga tgtcgatcgc   120

aaaattggct acatatggta tacaaaaaat tgcacccctg cctgcttacc caagaacaca   180

aaaattgtcg gccctgggaa atttggcacc aatgcagagg acggcaagat attacatgag   240

atggggggtc acttgtcgga ggtactacta ctttctttag tggtgctgtc cgacttcgca   300

ccggaaacag ctagtgtaat gtacctaatc ctacattttt ccatcccaca aagtcacgtt   360

gatgtaatgg attgtgataa gacccagttg aacctcacag tggagctgac aacagctgaa   420

gtaataccag ggtcggtctg gaatctaggc aaatatgtat gtataagacc aaaattggtgg   480

ccttatgaga caactgtagt gttggcattt gaagaggtga gccaggtggt gaagttagtg   540

ttgagggcac tcagagattt aacacgcatt tggaacgctg caacaactac tgctttttta   600

gtatgccttg ttaagatagt caggggccag atggtacagg gcattctgtg gctactattg   660

ataacagggg tacaagggca cttggattgc aaacctgaat tctcgtatgc catagcaaag   720

gacgaaagaa ttggtcaact gggggctgaa ggccttacca ccacttggaa ggaatactca   780

cctggaatga agctggaaga cacaatggtc attgcttggt gcgaagatgg gaagttaatg   840

tacctccaaa gatgcacgag agaaaccaga tatctcgcaa tcttgcatac aagagccttg   900

ccgaccagtg tggtattcaa aaaactcttt gatgggcgaa agcaagagga tgtagtcgaa   960

atgaacgaca actttgaatt tggactctgc ccatgtgatg ccaaacccat agtaagaggg   1020

aagttcaata caacgctgct gaacggaccg gccttccaga tggtatgccc cataggatgg   1080

acagggactg taagctgtac gtcattcaat atggacacct agccacaac tgtggtacgg   1140

acatatagaa ggtctaaacc attccctcat aggcaaggct gtatcaccca aaagaatctg   1200

ggggaggatc tccataactg catccttgga ggaaattgga cttgtgtgcc tggagaccaa   1260

ctactataca aggggggctc tattgaatct tgcaagtggt gtggctatca atttaaagag   1320

agtgagggac taccacacta ccccattggc aagtgtaaat ggagaacgaa gactggttac   1380

aggctagtag acagtacctc ttgcaataga gaaggtgtgg ccatagtacc acaagggaca   1440

ttaaagtgca agataggaaa aacaactgta caggtcatag ctatggatac caaactcgga   1500

cctatgcctt gcagaccata tgaaatcata tcaagtgagg ggcctgtaga aaagacagcg   1560

tgtactttca actacactaa gacattaaaa aataagtatt ttgagcccag agacagctac   1620

tttcagcaat acatgctaaa aggagagtat caatactggt ttgacctgga ggtgactgac   1680

catcaccggg attacttcgc tgagtccata ttagtggtgg tagtagccct cttgggtggc   1740

agatatgtac tttggttact ggttacatac atggtcttat cagaacagaa ggccttaggg   1800

tga   1803

<210>   26
<211>   600
<212>   PRT
<213>   Bovine viral diarrhea virus : deltaCE1E2

<400>   26

Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
1   5   10   15

Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Ala
            20   25   30

Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr Thr
        35   40   45

Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val Gly
    50   55   60

Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His Glu
65   70   75   80

Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val Leu
                85   90   95

Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu His
            100   105   110

Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys Thr
        115   120   125

Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro Gly
    130   135   140

Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp Trp
145   150   155   160

Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln Val
                165   170   175

Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp Asn
                180   185   190

Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val Arg
                195   200   205

Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly Val
                210   215   220

Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys
225   230   235   240

Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp
                245   250   255

Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala
                260   265   270

Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu
                275   280   285

Thr Arg Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val
                290   295   300

Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu
305   310   315   320

Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro
                325   330   335

Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe
                340   345   350

Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser
                355   360   365

```
Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg
    370             375             380

Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu
385             390             395             400

Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val
            405             410             415

Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys
            420             425             430

Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro
        435             440             445

Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp
    450             455             460

Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr
465             470             475             480

Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp
            485             490             495

Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser
            500             505             510

Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr
            515             520             525

Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr
    530             535             540

Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp
545             550             555             560

His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala
            565             570             575

Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val
            580             585             590

Leu Ser Glu Gln Lys Ala Leu Gly
```

595   600